



SEQUENCE LISTING

<110> ZHANG, HUANMIN
AX, ROY L
BELLIN, MARY E

<120> ISOLATED POLYNUCLEOTIDE SEQUENCES ENCODING A FERTILITY ASSOCIATED ANTIGEN

<130> 210707US20

<140> 09/905,114

<141> 2001-07-16

<150> US 60/218,140

<151> 2000-07-14

<160> 10

<170> PatentIn version 3.1

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<212> DNA

<213> Bos sp..

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att agc tct cgc ctt gga aga aac aca tat aaa gaa cag tat gcc ttt 96
Ile Ser Ser Arg Leu Gly Arg Asn Thr Tyr Lys Glu Gln Tyr Ala Phe
20 25 30

ctc tat aaa gaa aag cta gtg tct gta aaa caa agc tac ctc tac cac 144
Leu Tyr Lys Glu Lys Leu Val Ser Val Lys Gln Ser Tyr Leu Tyr His
35 40 45

gac tat cag gct gga gac gca gat gtg ttt tcc agg gaa ccc ttt gtg 192
Asp Tyr Gln Ala Gly Asp Ala Asp Val Phe Ser Arg Glu Pro Phe Val
50 55 60

gtc tgg ttc cag tca ccc tac acc gct gtc aag gac ttc gtg att gtc 240
Val Trp Phe Gln Ser Pro Tyr Thr Ala Val Lys Asp Phe Val Ile Val
65 70 75 80

ccc ctg cac acc acc cct gag aca tcc gtt aga gag att gat gag ctg 288
Pro Leu His Thr Thr Pro Glu Thr Ser Val Arg Glu Ile Asp Glu Leu
85 90 95

gct gat gtc tac aca gat gtg aaa cgt cgc tgg aat gca gag aat ttc 336
Ala Asp Val Tyr Thr Asp Val Lys Arg Arg Trp Asn Ala Glu Asn Phe
100 105 110

att ttc atg ggt gac ttc aat gct ggc tgc agc tac gtc ccc aag aag 384

Ile Phe Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr Val Pro Lys Lys
 115 120 125

gcc tgg aag gac atc cgc ctg agg acg gac ccc aag ttc gtt tgg ctg 432
 Ala Trp Lys Asp Ile Arg Leu Arg Thr Asp Pro Lys Phe Val Trp Leu
 130 135 140

atc ggg gac caa gag gac acc acg gtc aag aag agc aca aac tgc gcc 480
 Ile Gly Asp Gln Glu Asp Thr Thr Val Lys Lys Ser Thr Asn Cys Ala
 145 150 155 160

tat gac agg atc gtg ctt aga gga caa aat att gtc aac tct ggt ggt 528
 Tyr Asp Arg Ile Val Leu Arg Gly Gln Asn Ile Val Asn Ser Gly Gly
 165 170 175

cct caa tca aac ctc gtc ttt gat ttc cag aaa gct tac agg ttg tct 576
 Pro Gln Ser Asn Leu Val Phe Asp Phe Gln Lys Ala Tyr Arg Leu Ser
 180 185 190

gaa tcg aag gcc ctg g 592
 Glu Ser Lys Ala Leu
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Leu Tyr Lys Glu Lys Leu Val Ser Val Lys Gln Ser Tyr Leu Tyr His
 35 40 45

Asp Tyr Gln Ala Gly Asp Ala Asp Val Phe Ser Arg Glu Pro Phe Val
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Val Trp Phe Gln Ser Pro Tyr Thr Ala Val Lys Asp Phe Val Ile Val
 65 70 75 80

Pro Leu His Thr Thr Pro Glu Thr Ser Val Arg Glu Ile Asp Glu Leu
 85 90 95

Ala Asp Val Tyr Thr Asp Val Lys Arg Arg Trp Asn Ala Glu Asn Phe
 100 105 110

Ile Phe Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr Val Pro Lys Lys
 115 120 125

Ala Trp Lys Asp Ile Arg Leu Arg Thr Asp Pro Lys Phe Val Trp Leu
 130 135 140

Ile Gly Asp Gln Glu Asp Thr Thr Val Lys Lys Ser Thr Asn Cys Ala
 145 150 155 160

Tyr Asp Arg Ile Val Leu Arg Gly Gln Asn Ile Val Asn Ser Gly Gly
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Glu Ser Lys Ala Leu
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 ttctctataa agaaaagcta gtgtctgtaa aacaaagcta cctctaccac gactatcagg 180
 ctggagacgc agatgtgttt tccagggaaac cctttgtggc ctggttccag tcaccctaca 240
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 agattgatga gctggctgat gtctacacag atgtgaaacg tcgctggaat gcagagaatt 360
 tcattttcat ggggtgacttc aatgctggct gcagctacgt cccaagaag gcctggaagg 420
 acatccgcct gaggacggac cccaagttcg tttggctgat cggggaccaa gaggacacca 480
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25

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Ca
concord